CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/249,671A

CRF Processing Date: 3/4/96
Edited by: _____
Verified by: _____ Av _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☑ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____. **ENTERED**

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line.   SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.   3/1/95

```
┌─────────────────────────────────────────────────┐
│ This Raw Listing contains the General             │
│ Information Section and up to the first 5 pages.  │
└─────────────────────────────────────────────────┘
```

```
1                            SEQUENCE LISTING    ENTERED
2
3    (1)    General Information:
4
5           (i) APPLICANTS:      Hauptmann, R.
6                                Falkner, E.
7                                Bodo, G.
8                                VoÄ, T.
9                                Maurer-Fogy, I.
10
11          (ii) TITLE OF INVENTION:   Process for Preparing and Purifying
12                                     alpha-Interferon
13
14         (iii) NUMBER OF SEQUENCES: 11
15
16          (iv) CORRESPONDENCE ADDRESS:
17                  (A) ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
18                  (B) STREET:  1100 New York Avenue, Suite 600
19                  (C) CITY:  Washington
20                  (D) STATE:  D.C.
21                  (E) COUNTRY:  U.S.A.
22                  (F) ZIP:  20005
23
24           (v) COMPUTER READABLE FORM:
25                  (A) MEDIUM TYPE: Floppy disk
26                  (B) COMPUTER: IBM PC compatible
27                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
29
30          (vi) CURRENT APPLICATION DATA:
31                  (A) APPLICATION NUMBER: 08/249,671
32                  (B) FILING DATE: 26-MAY-1994
33                  (C) CLASSIFICATION:
34
35        (viii) ATTORNEY/AGENT INFORMATION:
36                  (A) NAME: Esmond, Robert W.
37                  (B) REGISTRATION NUMBER: 32,893
38                  (C) REFERENCE/DOCKET NUMBER: 0652.1350000
39
40          (ix) TELECOMMUNICATION INFORMATION:
41                  (A) TELEPHONE:  (202) 371-2600
42                  (B) TELEFAX:  (202) 371-2540
43
44
45
46    (2) INFORMATION FOR SEQ ID NO: 1:
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```
47
48          (i) SEQUENCE CHARACTERISTICS:
49               (A) LENGTH: 25 base pairs
50               (B) TYPE: nucleic acid
51               (C) STRANDEDNESS: both
52               (D) TOPOLOGY: unknown
53
54         (ii) MOLECULE TYPE: cDNA
55
56         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
57
58   CGTCTTCAAG AATTCGAGAT TATCG                          25
59
60   (2) INFORMATION FOR SEQ ID NO: 2:
61
62          (i) SEQUENCE CHARACTERISTICS:
63               (A) LENGTH: 56 base pairs
64               (B) TYPE: nucleic acid
65               (C) STRANDEDNESS: both
66               (D) TOPOLOGY: unknown
67
68         (ii) MOLECULE TYPE: cDNA
69
70
71
72         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
73
74   GACTTCAGAA GCTTCTGCAG TTACGATCGT TATCATTCCT TACTTCTTAA ACTTTC 56
75
76   (2) INFORMATION FOR SEQ ID NO: 3:
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78          (i) SEQUENCE CHARACTERISTICS:
79               (A) LENGTH: 35 base pairs
80               (B) TYPE: nucleic acid
81               (C) STRANDEDNESS: both
82               (D) TOPOLOGY: unknown
83
84         (ii) MOLECULE TYPE: cDNA
85
86
87
88         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
89
90   ATGCCTATGC ATGTGATCTG CCTCAAACCC ACAGC                35
91
92   (2) INFORMATION FOR SEQ ID NO: 4:
93
94          (i) SEQUENCE CHARACTERISTICS:
95               (A) LENGTH: 34 base pairs
96               (B) TYPE: nucleic acid
97               (C) STRANDEDNESS: both
98               (D) TOPOLOGY: unknown
99
```

```
100         (ii) MOLECULE TYPE: cDNA
101
102
103
104         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
105
106    GGCAGATCAC ATGCATAGGC ATTTGTAGCA ATAG                    34
107
108    (2) INFORMATION FOR SEQ ID NO: 5:
109
110         (i) SEQUENCE CHARACTERISTICS:
111              (A) LENGTH: 165 amino acids
112              (B) TYPE: amino acid
113              (D) TOPOLOGY: linear
114
115         (ii) MOLECULE TYPE: protein
116
117
118         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
119
120    Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
121    1             5                 10                  15
122
123    Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
124                20              25              30
125
126    Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
127            35              40              45
128
129    Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
130        50              55              60
131
132    Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
133    65              70              75              80
134
135    Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
136                85              90              95
137
138    Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
139                100             105             110
140
141    Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
142            115             120             125
143
144    Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
145        130             135             140
146
147    Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
148    145             150             155             160
149
150    Leu Arg Ser Lys Glu
151                165
152
```

```
153
154        (2) INFORMATION FOR SEQ ID NO: 6:
155
156            (i) SEQUENCE CHARACTERISTICS:
157                (A) LENGTH: 495 base pairs
158                (B) TYPE: nucleic acid
159                (C) STRANDEDNESS: both
160                (D) TOPOLOGY: unknown
161
162            (ii) MOLECULE TYPE: cDNA
163
164
165            (ix) FEATURE:
166                (A) NAME/KEY: CDS
167                (B) LOCATION: 1..495
168
169
170            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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172        TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG AGG ACC TTG ATG        48
173        Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
174         1                   5                  10                  15
175
176        CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC        96
177        Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
178                       20                  25                  30
179
180        AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA       144
181        Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
182                       35                  40                  45
183
184        AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC CAG CAG ATC TTC       192
185        Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
186               50                  55                  60
187
188        AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG GAT GAG ACC CTC       240
189        Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
190         65                  70                  75                  80
191
192        CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA       288
193        Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
194                       85                  90                  95
195
196        GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG       336
197        Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
198                      100                 105                 110
199
200        GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC       384
201        Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
202                      115                 120                 125
203
204        TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA       432
205        Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
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INPUT SET: S9110.raw

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206            130                135                140
207
208     GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT    480
209     Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
210     145                150                155                160
211
212     TTA AGA AGT AAG GAA                                                495
213     Leu Arg Ser Lys Glu
214                     165
215
216
217
218     (2) INFORMATION FOR SEQ ID NO: 7:
219
220         (i) SEQUENCE CHARACTERISTICS:
221             (A) LENGTH: 869 base pairs
222             (B) TYPE: nucleic acid
223             (C) STRANDEDNESS: both
224             (D) TOPOLOGY: unknown
225
226         (ii) MOLECULE TYPE: cDNA
227
228
229
230         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
231
232     GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG    60
233
234     TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC   120
235
236     GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA   180
237
238     AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT   240
239
240     GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTTATGAA AAAGAATATC   300
241
242     GCATTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT    360
243
244     CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG   420
245
246     AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG   480
247
248     TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG   540
249
250     ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC   600
251
252     AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG   660
253
254     GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC   720
255
256     TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT   780
257
258     GTCAGAGCAG AAATCATGAG ATCTTTTTCT TTGTCAACAA ACTTGCAAGA AAGTTTAAGA   840
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> This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.

```
 1                              SEQUENCE LISTING
 2
 3    (1)     General Information:
 4
 5         (i) APPLICANTS:      Hauptmann, R.
 6                              Falkner, E.
 7                              Bodo, G.
 8                              Voß, T.
 9                              Maurer-Fogy, I.
10
11        (ii) TITLE OF INVENTION:  Process for Preparing and Purifying
12                                  alpha-Interferon
13
14       (iii) NUMBER OF SEQUENCES: 11
15
16        (iv) CORRESPONDENCE ADDRESS:
17             (A) ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
18             (B) STREET:  1100 New York Avenue, Suite 600
19             (C) CITY:  Washington
20             (D) STATE:  D.C.
21             (E) COUNTRY:  U.S.A.
22             (F) ZIP:  20005
23
24         (v) COMPUTER READABLE FORM:
25             (A) MEDIUM TYPE: Floppy disk
26             (B) COMPUTER: IBM PC compatible
27             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28             (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
29
30        (vi) CURRENT APPLICATION DATA:
31             (A) APPLICATION NUMBER: 08/249,671
32             (B) FILING DATE: 26-MAY-1994
33             (C) CLASSIFICATION:
34
35      (viii) ATTORNEY/AGENT INFORMATION:
36             (A) NAME: Esmond, Robert W.
37             (B) REGISTRATION NUMBER: 32,893
38             (C) REFERENCE/DOCKET NUMBER: 0652.1350000
39
40        (ix) TELECOMMUNICATION INFORMATION:
41             (A) TELEPHONE:  (202) 371-2600
42             (B) TELEFAX:  (202) 371-2540
43
44
45
```

wrapped dept   **Does Not Comply**   **Corrected Diskette Needed**

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/249,671A*

DATE: 03/04/96
TIME: 15:06:03

INPUT SET: S9110.raw

ERRORED SEQUENCES FOLLOW:

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154          (2) INFORMATION FOR SEQ ID NO: 6:
155
156              (i) SEQUENCE CHARACTERISTICS:
-->  157              (A) LENGTH: 495 base pairs
158                  (B) TYPE: nucleic acid
159                  (C) STRANDEDNESS: both
160                  (D) TOPOLOGY: unknown
161
162              (ii) MOLECULE TYPE: cDNA
163
164
165              (ix) FEATURE:
166                  (A) NAME/KEY: CDS
167                  (B) LOCATION: 1..495
168
169
170              (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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172      TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG AGG ACC TTG ATG
173      48
174      Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
175       1               5                  10                  15
176
177      CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC
178      96
179      Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
180                  20                  25                  30
181
182      AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA
183      144
184      Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
185                  35                  40                  45
186
187      AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC CAG CAG ATC TTC
188      192
189      Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
190          50                  55                  60
191
192      AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG GAT GAG ACC CTC
193      240
194      Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
195          65                  70                  75                  80
196
197      CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA
198      288
199      Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
200                  85                  90                  95
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INPUT SET: S9110.raw

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202     GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG
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204     Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
205                 100                 105                 110
206
207     GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC
208     384
209     Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
210                 115                 120                 125
211
212     TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA
213     432
214     Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
215             130                 135                 140
216
217     GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT
218     480
219     Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
220     145                 150                 155                 160
221
222     TTA AGA AGT AAG GAA
223     495
224     Leu Arg Ser Lys Glu
225                         165
226
227
228
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229     (2) INFORMATION FOR SEQ ID NO: 7:
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231         (i) SEQUENCE CHARACTERISTICS:
232             (A) LENGTH: 869 base pairs
233             (B) TYPE: nucleic acid
234             (C) STRANDEDNESS: both
235             (D) TOPOLOGY: unknown
236
237         (ii) MOLECULE TYPE: cDNA
238
239
240
241         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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243     GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG
244     60
245
246     TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC
247     120
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249     GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA
250     180
251
252     AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT
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--> (line 232 indicator)

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256     300
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258     GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT
259     360
260
261     CTGCCTCAAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG
262     420
263
264     AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG
265     480
266
267     TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG
268     540
269
270     ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC
271     600
272
273     AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG
274     660
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276     GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC
277     720
278
279     TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT
280     780
281
282     GTCAGAGCAG AAATCATGAG ATCTTTTTCT TTGTCAACAA ACTTGCAAGA AAGTTTAAGA
283     840
284
285     AGTAAGGAAT GATAACGATC GTAACTGCA
286     869
287
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288     (2)  INFORMATION FOR SEQ ID NO: 8:
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290          (i)  SEQUENCE CHARACTERISTICS:
291                (A) LENGTH: 1177 base pairs
292                (B) TYPE: nucleic acid
293                (C) STRANDEDNESS: both
294                (D) TOPOLOGY: unknown
295
296          (ii) MOLECULE TYPE: cDNA
297
298
299          (ix) FEATURE:
300                (A) NAME/KEY: CDS
301                (B) LOCATION: 286..873
302                (D) OTHER INFORMATION: /function= "Cytokine"
303                        /product= "Interferon-omega1"
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INPUT SET: S9110.raw

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307               (B) LOCATION: 355..873
308               (D) OTHER INFORMATION: /function= "Cytokine"
309                   /product= "Interferon-omega"
310
311          (ix) FEATURE:
312               (A) NAME/KEY: sig_peptide
313               (B) LOCATION: 286..354
314               (D) OTHER INFORMATION: /product= "ST II Leader"
315
316          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
317
318   GAATTGGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG
319   60
320
321   TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC
322   120
323
324   GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA
325   180
326
327   AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT
328   240
329
330   GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTT ATG AAA AAG
331   294
332                                                   Met Lys Lys
333                                                   -23
334
335   AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA
336   342
337   Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
338   -20              -15              -10                       -5
339
340   AAT GCC TAT GCA TGT GAT CTG CCT CAG AAC CAT GGC CTA CTT AGC AGG
341   390
342   Asn Ala Tyr Ala Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg
343                       1            5                    10
344
345   AAC ACC TTG GTG CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT TTC TTG
346   438
347   Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu
348           15                  20                   25
349
350   TGT CTC AAG GAC AGA AGA GAC TTC AGG TTC CCC CAG GAG ATG GTA AAA
351   486
352   Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys
353           30                  35                   40
354
355   GGG AGC CAG TTG CAG AAG GCC CAT GTC ATG TCT GTC CTC CAT GAG ATG
356   534
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INPUT SET: S9110.raw

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361    582
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363                        65                    70                    75
364
365    TGG AAC ATG ACC CTC CTA GAC CAA CTC CAC ACT GGA CTT CAT CAG CAA
366    630
367    Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln
368                        80                    85                    90
369
370    CTG CAA CAC CTG GAG ACC TGC TTG CTG CAG GTA GTG GGA GAA GGA GAA
371    678
372    Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly Glu
373                    95                    100                   105
374
375    TCT GCT GGG GCA ATT AGC AGC CCT GCA CTG ACC TTG AGG AGG TAC TTC
376    726
377    Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe
378        110                   115                   120
379
380    CAG GGA ATC CGT GTC TAC CTG AAA GAG AAG AAA TAC AGC GAC TGT GCC
381    774
382    Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala
383    125                   130                   135                   140
384
385    TGG GAA GTT GTC AGA ATG GAA ATC ATG AAA TCC TTG TTC TTA TCA ACA
386    822
387    Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr
388                        145                   150                   155
389
390    AAC ATG CAA GAA AGA CTG AGA AGT AAA GAT AGA GAC CTG GGC TCA TCT
391    870
392    Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser
393                    160                   165                   170
394
395    TGAAATGATT CTCATTGATT AATTTGCCAT ATAACACTTG CACATGTGAC TCTGGTCAAT
396    930
397
398    TCAAAAGACT CTTATTTCGG CTTTAATCAC AGAATTGACT GAATTAGTTC TGCAAATACT
399    990
400
401    TTGTCGGTAT ATTAAGCCAG TATATGTTAA AAAGACTTAG GTTCAGGGGC ATCAGTCCCT
402    1050
403
404    AAGATGTTAT TTATTTTTAC TCATTTATTT ATTCTTACAT TTTATCATAT TTATACTATT
405    1110
406
407    TATATTCTTA TATAACAAAT GTTTGCCTTT ACATTGTATT AAGATAACAA AACATGTTCA
408    1170
409
410    GGATCCA
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PAGE: 7

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671A

DATE: 03/04/96
TIME: 15:06:14

INPUT SET: S9110.raw

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411        1177
412
413
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464        (2) INFORMATION FOR SEQ ID NO: 10:
465
466             (i) SEQUENCE CHARACTERISTICS:
467                 (A) LENGTH: 879 base pairs
468                 (B) TYPE: nucleic acid
469                 (C) STRANDEDNESS: both
470                 (D) TOPOLOGY: unknown
471
472            (ii) MOLECULE TYPE: cDNA
473
474
475
476            (ix) FEATURE:
477                 (A) NAME/KEY: CDS
478                 (B) LOCATION: 286..852
479
480            (ix) FEATURE:
481                 (A) NAME/KEY: mat_peptide
482                 (B) LOCATION: 355..852
483                 (D) OTHER INFORMATION: /function= "Cytokine"
484                     /product= "Interferon-alpha-2c"
485
486            (ix) FEATURE:
487                 (A) NAME/KEY: sig_peptide
488                 (B) LOCATION: 286..354
489                 (D) OTHER INFORMATION: /product= "ST II Leader"
490
491
492            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
493
494     GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG
495     60
496
497     TTGATTGATC AGGTAGAGGG GGCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC
498     120
499
500     GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA
501     180
502
503     AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT
504     240
505
506     GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTTGAGGTG ATTTT ATG AAA AAG
507     294
508                                                        Met Lys Lys
509                                                        -23
510
511     AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA
512     342
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INPUT SET: S9110.raw

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513        Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
514        -20             -15             -10                         -5
515
516        AAT GCC TAT GCA TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG
517        390
518        Asn Ala Tyr Ala Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg
519                          1               5                   10
520
521        AGG ACC TTG ATG CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC
522        438
523        Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser
524            15                  20                      25
525
526        TGC TTG AAG GAC AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC
527        486
528        Cys Leu Lys Asp Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly
529            30                  35                  40
530
531        AAC CAG TTC CAA AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC
532        534
533        Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile
534        45                  50                  55                  60
535
536        CAG CAG ATC TTC AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG
537        582
538        Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp
539                          65                  70                  75
540
541        GAT GAG ACC CTC CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG
542        630
543        Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu
544                80                  85                  90
545
546        AAT GAC CTG GAA GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT
547        678
548        Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr
549                95                  100                 105
550
551        CCC CTG ATG AAG GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA
552        726
553        Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln
554            110                 115                 120
555
556
557
558        AGA ATC ACT CTC TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG
559        774
560        Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp
561        125                 130                 135                 140
562
563        GAG GTT GTC AGA GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC
564        822
565        Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn
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INPUT SET: S9110.raw

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566                              145                 150                      155
567
568        TTG CAA GAA AGT TTA AGA AGT AAG GAA TGATAACGAT CGTAACTGCA
569        869
570        Leu Gln Glu Ser Leu Arg Ser Lys Glu
571                         160                 165
572
573        GAAGCTTAAT
574        879
575
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/249,671A*

INPUT SET: S9110.raw

Line	Error	Original Text
157	Entered (495) and Calc. Seq. Length (0) differ	(A) LENGTH: 495 base pairs
232	Entered (869) and Calc. Seq. Length (0) differ	(A) LENGTH: 869 base pairs
291	Entered (1177) and Calc. Seq. Length (0) differ	(A) LENGTH: 1177 base pairs
467	Entered (879) and Calc. Seq. Length (0) differ	(A) LENGTH: 879 base pairs